

MARKED-UP VERSION OF AMENDMENTS

JC675 U.S. PTO
10/007132
12/03/01

Additions to the text are indicated by double underlining;
deletions are indicated by square brackets.

In the Specification:

The replacement title on page 1, lines 4-5, and on page 236,
line 1:

--[DNA ENCODING GALANIN GALR3 RECEPTORS AND USES THEREOF]
PROCESSES FOR PREPARING COMPOSITIONS INVOLVING GALR3
RECEPTOR SPECIFIC COMPOUNDS--

The replacement paragraph on page 1, after the title:

-- This application is a continuation of U.S. Serial No. 09/058,333, filed April 9, 1998, now allowed, which is a continuation-in-part of PCT International Application No. PCT/US97/18222, filed October 9, 1997, which is a continuation-in-part [in the U.S.] and claims priority of U.S. Serial No. 08/900,230, filed July 23, 1997, now allowed, which is a continuation-in-part of U.S. Serial No. 08/787,261, filed January 24, 1997, now abandoned, which is a continuation-in-part of U.S. Serial No. 08/767,964, filed December 17, 1996, now abandoned, which is a continuation-in-part of U.S. Serial No. 08/728,139, filed October 9, 1996, now abandoned, the contents of which are incorporated by reference. Throughout this application, various references are referred to within parentheses. Disclosures of these publications in their entireties are hereby incorporated by reference into this application to more fully describe the state of the art to which this invention pertains. Full bibliographic citation for these references may be found at the end of this application, preceding the

Applicants: Jonathan A. Bard
Serial No: Not Yet Known
Filed: Herewith
Exhibit 1

sequence listing and the claims. --

The replacement paragraph on page 8, line 33 through page 9, line 9:

--This invention provides a nucleic acid probe comprising at least 15 nucleotides, which probe specifically hybridizes with a nucleic acid encoding a GALR3 receptor, wherein the probe has a unique sequence corresponding to a sequence present within one of the two strands of the nucleic acid encoding the GALR3 receptor contained in plasmid K1086. This invention still further provides a nucleic acid probe comprising 15 nucleotides, which probe specifically hybridizes with a nucleic acid encoding a GALR3 receptor, wherein the probe has a unique sequence corresponding to a sequence present within (a) the nucleic acid sequence described in Figure 1 ([Seq. ID No. 1] SEQ ID NO: 1) or (b) the reverse complement to the nucleic acid sequence shown in Figure 1 ([Seq. ID No. 1] SEQ ID NO: 1).--

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The replacement paragraph on page 9, lines 11-33:

--In yet another embodiment, the GALR3 receptor is the rat GALR3 receptor having substantially the same amino acid sequence as the amino acid sequence shown in Figure 2. In another embodiment, the GALR3 receptor is the rat GALR3 receptor having the amino acid sequence shown in Figure 2. In another embodiment, the GALR3 receptor is the human GALR3 receptor. In another embodiment, the GALR3 receptor is the human GALR3 receptor encoded by the coding sequence of plasmid pEXJ-hGalR3. This invention also provides a nucleic acid probe comprising at least 15 nucleotides, which probe specifically hybridizes with a nucleic acid

encoding a GALR3 receptor, wherein the probe has a unique sequence corresponding to a sequence present within one of the two strands of the nucleic acid encoding the GALR3 receptor contained in plasmid pEXJ-hGalR3. This invention provides a nucleic acid probe comprising at least 15 nucleotides, which probe specifically hybridizes with a nucleic acid encoding a GALR3 receptor, wherein the probe has a unique sequence corresponding to a sequence present within (a) the nucleic acid sequence described in Figure 3 ([Seq. ID No. 3] SEQ ID NO: 3) or (b) the reverse complement to the nucleic acid sequence shown in Figure 3 ([Seq. ID No. 3] SEQ ID NO: 3).--

The replacement paragraph on page 24, lines 3-6:

--**Figure 1** Nucleotide coding sequence of the rat hypothalamic galanin GALR3 receptor ([Seq. I.D. No. 1] SEQ ID NO: 1), with partial 5' and 3' untranslated sequences. Start and stop codons are underlined.--

The replacement paragraph on page 24, lines 7-10:

--**Figure 2** Deduced amino acid sequence of the rat hypothalamic galanin GALR3 receptor ([Seq. I.D. No. 2] SEQ ID NO: 2) encoded by the rat nucleotide sequence shown in Figure 1.--

The replacement paragraph on page 24, lines 12-15:

--**Figure 3** Nucleotide coding sequence of the human galanin GALR3 receptor ([Seq. I.D. No. 3] SEQ ID NO: 3), with partial 5' and 3' untranslated sequences. Start and stop codons are underlined.--

The replacement paragraph on page 24, lines 17-22:

--**Figure 4** Deduced amino acid sequence of the human galanin GALR3 receptor ([Seq. I.D. No. 4] SEQ ID NO: 4) encoded by the human nucleotide sequence shown in Figure 3.--

The replacement paragraph on page 24, lines 24-29:

--**Figures 5A-5D** Amino acid sequence alignment of the rat GALR3 receptor (top row) ([Seq. ID No. 2] SEQ ID NO: 2), human GALR3 receptor (middle row) ([Seq. ID No. 4] SEQ ID NO: 4) and rat GALR1 receptor (bottom row) ([Seq. ID No. 5] SEQ ID NO: 5). Transmembrane domains (TM 1-7) are indicated by brackets above the sequence.--

The replacement paragraph on page 29, line 13 through page 30, line 3:

---This invention provides an isolated nucleic acid encoding a GALR3 receptor having the same or substantially the same amino acid sequence as the amino acid sequence encoded by the plasmid K1086 (ATCC Accession No. 97747). In an embodiment, the nucleic acid is DNA. This invention further provides an isolated nucleic acid encoding a rat GALR3 receptor having the amino acid sequence encoded by the plasmid K1086. This invention provides an isolated nucleic acid encoding a GALR3 receptor having the same or substantially the same amino acid sequence as the amino acid sequence encoded by the plasmid pEXJ-RGalR3T (ATCC Accession No. 97826). In an embodiment, the nucleic acid is DNA. This invention further provides an isolated nucleic acid encoding a rat GALR3 receptor having the amino acid sequence encoded by the plasmid pEXJ-RGalR3T (ATCC Accession No. 97826). This invention provides an isolated nucleic acid encoding a GALR3 receptor having substantially the same amino acid sequence as the amino acid sequence shown in Figure 2 ([Seq. I.D. No. 2] SEQ ID NO: 2). In

another embodiment, the GALR3 receptor is the rat GALR3 receptor having the amino acid sequence shown in Figure 2 ([Seq. ID No. 2] SEQ ID NO: 2). In another embodiment, the nucleic acid comprises at least an intron. In still another embodiment, the nucleic acid comprises alternately spliced nucleic acid transcribed from the nucleic acid contained in plasmid K1086. In an embodiment, the alternately spliced nucleic acid is mRNA transcribed from DNA encoding a galanin receptor.--

The replacement paragraph on page 30, lines 5-18:

---In an embodiment, the GALR3 receptor is a human GALR3 receptor. This invention provides an isolated nucleic acid encoding a human GALR3 receptor having the same or substantially the same amino acid sequence as the amino acid sequence encoded by plasmid pEXJ-hGalR3 (ATCC Accession No. 97827). This invention provides an isolated nucleic acid encoding a human GALR3 receptor, wherein the human GALR3 receptor has a sequence, which sequence comprises substantially the same amino acid sequence as the sequence shown in Figure 4 ([Seq. I.D. No. 4] SEQ ID NO: 4) from amino acid 60 through amino acid 427. In another embodiment, the GALR3 receptor has a sequence, which sequence comprises the sequence shown in Figure 4 ([Seq. ID No. 4] SEQ ID NO: 4) from amino acid 60 through amino acid 427.--

The replacement paragraph on page 34, line 33 through page 35, line 10:

--This invention also provides an isolated galanin GALR3 receptor protein. In one embodiment, the GALR3 receptor protein has the same or substantially the same amino acid sequence as the amino acid sequence encoded by plasmid

K1086. In another embodiment, the GALR3 receptor protein has the amino acid sequence encoded by plasmid K1086. In another embodiment, the protein has the amino acid sequence encoded by the plasmid pEXJ-hGalR3. In an embodiment, the GALR3 receptor protein has the same or substantially the same amino acid sequence as the amino acid sequence shown in Figure 2 ([Seq. I.D. No. 2] SEQ ID NO: 2). In an embodiment, the GALR3 receptor comprises the same or substantially the same amino acid sequence as the amino acid sequence shown in Figure 4 ([Seq. I.D. No. 4] SEQ ID NO: 4) from amino acid 60 through amino acid 427.--

The replacement paragraph on page 38, lines 29-30:

--This invention provides a plasmid designated M67 (ATCC [Accession] Designation No. 209708).--

The replacement paragraph on page 38, line 32 through page 39, line 1:

--This plasmid (M67) was deposited on March 27, 1998, with the American Type Culture Collection (ATCC), [12301 Parklawn Drive, Rockville, Maryland 20852,] 10801 University Blvd., Manassas, Virginia 20110-2209, U.S.A. under the provisions of the Budapest Treaty for the International Recognition of the Deposit of Microorganisms for the Purposes of Patent Procedure and was accorded ATCC [Accession] Designation No. [xxxxx] 209708.--

The replacement paragraph on page 40, line 35 through page 41, line 5:

---This invention still further provides a nucleic acid probe comprising at least 15 nucleotides, which probe specifically hybridizes with a nucleic acid encoding a GALR3 receptor, wherein the probe has a unique sequence

corresponding to a sequence present within (a) the nucleic acid sequence shown in Figure 1 ([Seq. ID No. 1] SEQ ID NO: 1) or (b) the reverse complement to the nucleic acid sequence shown in Figure 1 ([Seq. ID No. 1] SEQ ID NO: 1).--

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The replacement paragraph on page 41, lines 7-20:

--This invention also provides a nucleic acid probe comprising at least 15 nucleotides, which probe specifically hybridizes with a nucleic acid encoding a GALR3 receptor, wherein the probe has a unique sequence corresponding to a sequence present within one of the two strands of the nucleic acid encoding the GALR3 receptor contained in plasmid pEXJ-hGalR3. This invention provides a nucleic acid probe comprising at least 15 nucleotides, which probe specifically hybridizes with a nucleic acid encoding a GALR3 receptor, wherein the probe has a unique sequence corresponding to a sequence present within (a) the nucleic acid sequence shown in Figure 3 ([Seq. ID No. 3] SEQ ID NO: 3) or (b) the reverse complement to the nucleic acid sequence shown in Figure 3 ([Seq. ID No. 3] SEQ ID NO: 3).--

The replacement paragraph on page 48, line 16 through 49, line 15:

--In one embodiment, the GALR3 receptor is a mammalian GALR3 receptor. In another embodiment, the GALR3 receptor is a rat GALR3 receptor. In still another embodiment, the GALR3 receptor has the same or substantially the same amino acid sequence as that encoded by plasmid K1086. In still another embodiment, the GALR3 receptor has the amino acid sequence encoded by plasmid K1086. In another embodiment, the GALR3 receptor has substantially the same amino acid

sequence as the amino acid sequence shown in Figure 2 ([Seq. ID No. 2] SEQ ID NO: 2). In another embodiment, the GALR3 receptor has the amino acid sequence shown in Figure 2 ([Seq. ID No. 2] SEQ ID NO: 2). In still another embodiment, the cells are transfected with the plasmid pEXJ-RGALR3T (ATCC Accession No. 97826), encoding the rat GALR3 receptor. Plasmid pEXJ-RGalR3T comprises the entire coding region of rat GALR3, but in which the 5' initiating ATG is joined directly to the vector, and which comprises only 100 nucleotides from the 3' untranslated region after the stop codon (i.e., up to and including nucleotide 1275 in Figure 1 ([Seq. ID NO. 1] SEQ ID NO: 1)). Transfection of cells with the "trimmed" plasmid results in a higher level of expression of the rat GALR3 receptor than the level of expression when plasmid K1086 is used. The use of the "trimmed" plasmid provides for greater convenience and accuracy in binding assays. In another embodiment the GALR3 receptor is a human GALR3 receptor. In still another embodiment, the GALR3 receptor has the same or substantially the same amino acid sequence as that encoded by plasmid pEXJ-hGalR3 (ATCC Accession No. 97827). In an embodiment, the human GALR3 receptor has a sequence, which sequence comprises substantially the same amino acid sequence as the sequence shown in Figure 4 ([Seq. I.D. No. 4] SEQ ID NO: 4) from amino acid 60 through amino acid 427. In another embodiment, the GALR3 receptor has a sequence, which sequence comprises the sequence shown in Figure 4 ([Seq. ID No. 4] SEQ ID NO: 4) from amino acid 60 through amino acid 427.--

The replacement paragraph on page 50, line 17 through 51, line 4:

---In one embodiment, the GALR3 receptor is a rat GALR3 receptor. In another embodiment, the GALR3 receptor has

the same or substantially the same amino acid sequence as that encoded by the plasmid K1086. In yet another embodiment, the GALR3 receptor has the amino acid sequence encoded by the plasmid K1086. In another embodiment, the GALR3 receptor has substantially the same amino acid sequence as the amino acid sequence shown in Figure 2 ([Seq. ID No. 2] SEQ ID NO: 2). In another embodiment, the GALR3 receptor has the amino acid sequence shown in Figure 2 ([Seq. ID No. 2] SEQ ID NO: 2). In another embodiment, the GALR3 receptor is a human GALR3 receptor. In still another embodiment, the GALR3 receptor has the same or substantially the same amino acid sequence as that encoded by plasmid pEXJ-hGalR3 ATCC Accession No. 97827). In another embodiment, the human GALR3 receptor has a sequence, which sequence comprises substantially the same amino acid sequence as the sequence shown in Figure 4 ([Seq. I.D. No. 4] SEQ ID NO: 4) from amino acid 60 through amino acid 427. In another embodiment, the GALR3 receptor has a sequence, which sequence comprises the sequence shown in Figure 4 ([Seq. ID No. 4] SEQ ID NO: 4) from amino acid 60 through amino acid 427. In another embodiment of this invention the cells are transfected with plasmid pEXJ-RGalR3T (ATCC Accession No. 97826).--

The replacement paragraph on page 51, line 29 through 52, line 15:

---In an embodiment, the GALR3 receptor is a mammalian GALR3 receptor. In one embodiment of the invention, the GALR3 receptor is a rat GALR3 receptor. In another embodiment, the GALR3 receptor has the same or substantially the same amino acid sequence as that encoded by the plasmid K1086. In still another embodiment, the GALR3 receptor has the amino acid sequence encoded by the plasmid K1086. In another embodiment, the GALR3 receptor

has substantially the same amino acid sequence as the amino acid sequence shown in Figure 2 ([Seq. ID No. 2] SEQ ID NO: 2). In another embodiment, the GALR3 receptor has the amino acid sequence shown in Figure 2 ([Seq. ID No. 2] SEQ ID NO: 2). In another embodiment, the GALR3_receptor is a human GALR3 receptor. In still another embodiment, the GALR3 receptor has the same or substantially the same amino acid sequence as that encoded by plasmid pEXJ-hGalR3 ATCC Accession No. 97827). In another embodiment, the human GALR3 receptor has a sequence, which sequence comprises substantially the same amino acid sequence as the sequence shown in Figure 4 ([Seq. I.D. No. 4] SEQ ID NO: 4) from amino acid 60 through amino acid 427. In another embodiment, the GALR3 receptor has a sequence, which sequence comprises the sequence shown in Figure 4 ([Seq. ID No. 4] SEQ ID NO: 4) from amino acid 60 through amino acid 427.--

The replacement paragraph on page 53, lines 17-19:

--In an embodiment of any of the above processes, the cells are injected with RNA synthesized in vitro from the plasmid designated M67 (ATCC [Accession] Designation No. 209708).--

The replacement paragraph on page 58, line 34 through 59, line 21:

---In an embodiment of any of the above processes, the GALR3 receptor is a mammalian GALR3 receptor. In another embodiment of the above processes, the GALR3 receptor is a rat GALR3 receptor or a human GALR3 receptor. In still another embodiment of the above processes, the GALR3 receptor has the same or substantially the same amino acid sequence as encoded by the plasmid K1086 (ATCC Accession

No. 97747). In another embodiment, the GALR3 receptor has substantially the same amino acid sequence as the amino acid sequence shown in Figure 2 ([Seq. ID No. 2] SEQ ID NO: 2). In another embodiment, the GALR3 receptor has the amino acid sequence shown in Figure 2 ([Seq. ID No. 2] SEQ ID NO: 2). In still another embodiment, the GALR3 receptor has the same or substantially the same amino acid sequence as that encoded by plasmid pEXJ-hGalR3 (ATCC Accession No. 97827). In another embodiment, the human GALR3 receptor has a sequence, which sequence comprises substantially the same amino acid sequence as the sequence shown in Figure 4 ([Seq. I.D. No. 4] SEQ ID NO: 4) from amino acid 60 through amino acid 427. In another embodiment, the GALR3 receptor has a sequence, which sequence comprises the sequence shown in Figure 4 ([Seq. ID No. 4] SEQ ID NO: 4) from amino acid 60 through amino acid 427. In another embodiment of this invention the cells are transfected with plasmid pEXJ-RGalR3T (ATCC Accession No. 97826).--

The replacement paragraph on page 61, line 20 through 62, line 5:

---In an embodiment of any of the above processes, the GALR3 receptor is a mammalian GALR3 receptor. In an embodiment of the above-described methods, the GALR3 receptor is a rat GALR3 receptor. In another embodiment, the GALR3 receptor has the same or substantially the same amino acid sequence as the amino acid sequence encoded by plasmid K1086. In another embodiment, the GALR3 receptor has substantially the same amino acid sequence as the amino acid sequence shown in Figure 2 ([Seq. ID No. 2] SEQ ID NO: 2). In another embodiment, the GALR3 receptor has the amino acid sequence shown in Figure 2 ([Seq. ID No. 2] SEQ ID NO: 2). In another embodiment, the GALR3 receptor is a human GALR3 receptor. In still another embodiment, the

GALR3 receptor has the same or substantially the same amino acid sequence as that encoded by plasmid pEXJ-hGalR3 (ATCC Accession No. 97827). In another embodiment, the human GALR3 receptor has a sequence, which sequence comprises substantially the same amino acid sequence as the sequence shown in Figure 4 ([Seq. ID No. 4] SEQ ID NO: 4) from amino acid 60 through amino acid 427. In another embodiment, the GALR3 receptor has a sequence, which sequence comprises the sequence shown in Figure 4 ([Seq. I.D. No. 4] SEQ ID NO: 4) from amino acid 60 through amino acid 427. In another embodiment, the GALR3 receptor has a sequence, which sequence comprises the sequence shown in Figure 4 ([Seq. ID No. 4] SEQ ID NO: 4) from amino acid 60 through amino acid 427.--

The replacement paragraph on page 63, lines 5-26:

---In an embodiment of any of the above-described methods, the GALR3 receptor is a rat GALR3 receptor. In still another embodiment, the GALR3 receptor has the same or substantially the same amino acid sequence as the amino acid sequence encoded by plasmid K1086. In another embodiment, the GALR3 receptor has substantially the same amino acid sequence as the amino acid sequence shown in Figure 2 ([Seq. ID No. 2] SEQ ID NO: 2). In another embodiment, the GALR3 receptor has the amino acid sequence shown in Figure 2 ([Seq. ID No. 2] SEQ ID NO: 2). In another embodiment, the GALR3 receptor is a human GALR3 receptor. In still another embodiment, the GALR3 receptor has the same or substantially the same amino acid sequence as that encoded by plasmid pEXJ-hGalR3 (ATCC Accession No. 97827). In another embodiment, the GALR3 receptor has a sequence, which sequence comprises the sequence shown in Figure 4 ([Seq. ID No. 4] SEQ ID NO: 4) from amino acid 60 through amino acid 427. In another embodiment, the GALR3

receptor has a sequence, which sequence comprises the sequence shown in Figure 4 ([Seq. ID No. 4] SEO ID NO: 4) from amino acid 60 through amino acid 427.--

The replacement paragraph on page 64, line 33 through page 65, line 26:

--In an embodiment of any of the above-described methods, the GALR3 receptor is a rat GALR3 receptor. In another embodiment, the GALR3 receptor has the same or substantially the same amino acid sequence as the amino acid sequence encoded by plasmid K1086. In another embodiment, the GALR3 receptor has substantially the same amino acid sequence as the amino acid sequence shown in Figure 2 ([Seq. ID No. 2] SEO ID NO: 2). In another embodiment, the GALR3 receptor has the amino acid sequence shown in Figure 2 ([Seq. ID No. 2] SEO ID NO: 2). In another embodiment, the GALR3 receptor is a human GALR3 receptor. In still another embodiment, the GALR3 receptor has the same or substantially the same amino acid sequence as that encoded by plasmid pEXJ-hGalR3 (ATCC Accession No. 97827). In still another embodiment, the GALR3 receptor has the same or substantially the same amino acid sequence as that encoded by plasmid pEXJ-RGalR3T (ATCC Accession No. 97826). In still another embodiment, the GALR3 receptor has the same or substantially the same amino acid sequence as that encoded by plasmid M54 (ATCC Accession No. 209312). In still another embodiment, the GALR3 receptor has the same or substantially the same amino acid sequence as that encoded by plasmid M67 (ATCC [Accession] Designation No. 209708). In another embodiment, the human GALR3 receptor has a sequence, which sequence comprises substantially the same amino acid sequence as the sequence shown in Figure 4 ([Seq. I.D. No. 4] SEO ID NO: 4) from amino acid 60 through amino acid 427. In another embodiment, the GALR3 receptor

has a sequence, which sequence comprises the sequence shown in Figure 4 ([Seq. ID NO. 4] SEQ ID NO: 4) from amino acid 60 through amino acid 427.--

The replacement paragraph on page 68, line 32 through page 69, line 15:

--In an embodiment of any of the above-described processes, the GALR3 receptor is a mammalian GALR3 receptor. In another embodiment of any of the above-described processes, the GALR3 receptor has substantially the same amino acid as encoded by the plasmid K1086 (ATCC Accession No. 97747). In another embodiment of any of the above-described processes, the GALR3 receptor has substantially the same amino acid sequence as that shown in Figure 2 ([Seq. ID NO. 2] SEQ ID NO: 2). In still another embodiment of any of the above-described processes, the GALR3 receptor has substantially the same amino acid sequence as encoded by the plasmid pEXJ-hGalR3 (ATCC Accession No. 97827). In an embodiment of any of the above-described processes, the GALR3 receptor has a sequence, which sequence comprises substantially the same amino acid sequence as that shown in Figure 4 ([Seq. ID NO. 4] SEQ ID NO: 4) from amino acid 60 through amino acid 427. In still another embodiment of any of the above-described processes, the GALR3 receptor has a sequence, which sequence comprises a sequence shown in Figure 4 ([Seq. ID NO. 4] SEQ ID NO: 4) from amino acid 60 through amino acid 427.--

The replacement paragraph on page 98, lines 7-18:

--Human brain multiple tissue northern blots (MTN brain blots II and III, Clontech, Palo Alto, CA) and human peripheral MTN blot (Clontech, Palo Alto, CA) carrying mRNA

(2 µg) purified from various human brain areas and peripheral tissues, respectively, were hybridized at high stringency with overlapping probes directed to the amino-terminus of hGALR3

5' GATGGCTGATGCCCAGAACATTTCACTGGACAGCCCAGGGAGTGT 3'

([SEQ ID NO. 51] SEQ ID NO: 51) and

5' GACCACAGGCACTGCCACGGCCCCACACTCCCTGGGCTGTCCAG 3'

([SEQ ID NO. 52] SEQ ID NO: 52), according to the manufacturer's specifications.--

The replacement paragraph on page 98, lines 21-34:

--Tissues were homogenized and total RNA extracted using the guanidine isothiocyanate/CsCl cushion method. RNA was then treated with DNase to remove any contaminating genomic DNA and poly A⁺-selected using FastTrack kit (Invitrogen), according to manufacturer's specifications. cDNA was prepared from mRNA with random hexanucleotide primers using reverse transcriptase Superscript II (BRL, Gaithersburg, MD). First strand cDNA (corresponding to ≈5 ng of poly A⁺ RNA) was amplified in a 50 µL PCR reaction mixture with 300 nM of forward (directed to the amino-terminus: ([SEQ ID NO. 24] SEQ ID NO: 24) and reverse (directed to the third intracellular loop: ([SEQ ID NO. 27] SEQ ID NO: 27)) primers, using the thermal cycling program and conditions described above.--

The replacement paragraph on page 98, line 37 through page 99, line 13:

--The PCR products were run on a 1.5% agarose gel and transferred to charged nylon membranes (Zetaprobe GT, BioRad), and analyzed as Southern blots. GALR3 primers were screened for the absence of cross-reactivity with the other galanin receptors. Filters were hybridized with a

radiolabeled probe directed to the first intracellular loop,

5'-TGCAGCCTGGCCCAAGTGCCTGGCAGGAGCCAAGCAGTACCACAG-3' ([Seq. I.D. No. 53] SEQ ID NO: 53), and washed under high stringency. Labeled PCR products were visualized on X-ray film. Similar PCR and Southern blot analyses were conducted with primers and probes directed to the housekeeping gene, glyceraldehyde phosphate dehydrogenase (G3PDH; Clontech, Palo Alto, CA), to normalize the amount of cDNA used from the different tissues.--

The replacement paragraph on page 99, lines 15-27:

--RT-PCR was performed on human pituitary cDNA (two sources: Clontech cDNA and cDNA prepared from poly A+RNA purchased from ABS) using the following conditions: 94°C for 30 sec and 68°C for 2 min, for 40 cycles, with a preincubation at 94°C for 2 min and a postincubation at 68°C for 5 minutes. Primers specific for human GALR1 were used (KS1177; [SEQ ID NO. 35] SEQ ID NO: 35 and KS1178; [SEQ ID NO. 36] SEQ ID NO: 36). Primers specific for human GALR2 were used (BB183; [SEQ ID NO. 60] SEQ ID NO: 60 and BB184; [SEQ ID NO. 61] SEQ ID NO: 61). Primers specific for human GALR3 were used (BB444; [SEQ ID NO. 62] SEQ ID NO: 62 and BB445; [SEQ ID NO. 63] SEQ ID NO: 63). Primers specific for human prolactin were used (BB446; [SEQ ID NO. 64] SEQ ID NO: 64 and BB447; [SEQ ID NO. 65] SEQ ID NO: 65).--

The replacement paragraph on page 99, line 31 through page 100, line 8:

--BB183: 5'-TCAGCGGCACCATGAACGTCTCGGGCT-3' ([SEQ ID NO. 60] SEQ ID NO: 60).

BB184: 5'-GGCCACATCAACCGTCAGGATGCT-3' ([SEQ ID NO. 61]

SEQ ID NO: 61)

BB444: 5'-ATGGCTGATGCCCAGAACATTTTCAC-3' ([SEQ ID NO. 62]
SEQ ID NO: 62) .

BB445: 5'-TAGCGCACGGTGCCGTAGTAGCTGAGGT-3' ([SEQ ID NO.
63] SEQ ID NO: 63) .

BB446: 5'-ATGAAAGGGTCCCTCCTGCTGCTGCT-3' ([SEQ ID NO. 64]
SEQ ID NO: 64) .

BB447: 5'-TATCAGCTCCATGCCCTCTAGAAGCC-3' ([SEQ ID NO. 65]
SEQ ID NO: 65) .--

The replacement paragraph on page 110, line 22 through page 112,
line 10:

--Oocytes were isolated as described above, except that 3
mg/mL collagenase was used to defolliculate the oocytes.
Genes encoding G-protein inwardly rectifying K⁺ channels 1
and 4 (GIRK1 and GIRK4) were obtained by PCR using the
published sequences (Kubo et al., 1993; Dascal et al.,
1993; Krapivinsky et al., 1995b) to derive appropriate 5'
and 3' primers. Human heart cDNA was used as template
together with the primers

5'-CGCGGATCCATTATGTCTGCACTCCGAAGGAAATTTG-3' (SEQ ID NO[.]54) and

5'-CGCGAATTCTTATGTGAAGCGATCAGAGTTCATTTTTC -3' (SEQ ID
NO[.]55) for GIRK1 and

5'-GCGGGATCCGCTATGGCTGGTGATTCTAGGAATG-3' (SEQ ID NO[.]56)
and

5'- CCGGAATTCCCCTCACACCGAGCCCCTGG-3' (SEQ ID NO[.]57) for
GIRK4. In each primer pair, the upstream primer contained
a BamHI site and the downstream primer contained an EcoRI
site to facilitate cloning of the PCR product into pcDNA1-
Amp (Invitrogen). The transcription template for hGalR3
was obtained similarly by PCR using the cloned cDNA in

combination with primers

5'-CCAAGCTTCTAATACGACTCACTATAGGGCCACCATGGCTGATGCCAGA-3'
(SEQ ID NO[.]58) and

5'-TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTGCAGG

TTTATTCCGGTCCTCG-3' (SEQ ID NO[.]59). Alternatively, the complete coding region of hGalR3 is subcloned into the high-efficiency transcription vector pBS KS⁺ AMV-pA50 (Nowak et al., 1995). This plasmid was modified by adding the recognition sequence for the restriction enzyme SrfI downstream of the poly A sequence in the plasmid. The new plasmid was designated M52. Subcloning involved the isolation of a 1.1 kb NcoI/EcoRI restriction fragment encoding the entire hGALR3 gene followed by its ligation into NcoI/EcoRI digested M52. After identification of a suitable clone (M54), the transcription template was produced by linearization of the plasmid DNA with SrfI. The plasmid M54 was deposited on September 30, 1997, with the American Type Culture Collection (ATCC), 12301 Parklawn Drive, Rockville, Maryland 20852, U.S.A. under the provisions of the Budapest Treaty for the International Recognition of the Deposit of Microorganisms for the Purposes of Patent Procedure and was accorded ATCC Accession No. 209312. The sequence comprising the coding region of rat GALR3 was subcloned into pBS KS⁺AMV-pA50 (Nowak, et al., 1995) to produce M67. The transcription template was produced by linearization of the plasmid DNA with SrfI. The plasmid M67 was deposited on March 27, 1998, with the American Type Culture Collection (ATCC), [12301 Parklawn Drive, Rockville, Maryland 20852,] 10801 University Blvd., Manassas, Virginia 20110-2209, U.S.A. under the provisions of the Budapest Treaty for the International Recognition of the Deposit of Microorganisms for the Purposes of Patent Procedure and was accorded ATCC [Accession] Designation No. [xxxxxxx] 209708. mRNAs were transcribed using the T7 polymerase ("Message Machine", Ambion). Each oocyte received 2 ng each of GIRK1 and GIRK4

mRNA in combination with 25 ng of GalR3 mRNA. In other experiments oocytes received injections of mRNAs encoding the human $\alpha 1A$ adrenergic receptor, rGalR1 or rGalR2 galanin receptors (Forray et al., 1994; Parker et al., 1995) with or without GIRKs 1 and 4. After injection of mRNAs, oocytes were incubated at 17° for 3-8 days.--

The replacement paragraph on page 156, lines 12-23:

--The human GALR3 gene contains two in-frame METs: the first (as one reads 5' to 3') will be referred to herein as the "upstream MET" and the second (i.e., closer to TM1) will be referred to herein as the "downstream MET." Both the upstream and downstream METs are shown in Figure 4 ([Seq. ID No. 4] SEQ ID NO: 4). Based on data currently available, it is believed that the downstream MET is likely to be the correct initiating methionine. It is theoretically possible that the upstream MET might be the initiating MET. It is to be understood that the present invention includes both the receptor beginning at the downstream MET and the receptor beginning at the upstream MET.--

SEQUENCE LISTING

JC675 U.S. PTO
10/007132
12/03/01

(1) GENERAL INFORMATION:

- (i) APPLICANT: Bard, Jonathan A
Borowsky, Beth
Smith, Kelli E
- (ii) TITLE OF INVENTION: DNA ENCODING GALANIN GALR3 RECEPTORS
AND USES THEREOF
- (iii) NUMBER OF SEQUENCES: 65
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Cooper & Dunham LLP
 - (B) STREET: 1185 Avenue of the Americas
 - (C) CITY: New York
 - (D) STATE: New York
 - (E) COUNTRY: U.S.A.
 - (F) ZIP: 10036
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: White, John P
 - (B) REGISTRATION NUMBER: 28,678
 - (C) REFERENCE/DOCKET NUMBER: 52241-E/JPW/KDB
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 212 278 0400
 - (B) TELEFAX: 212 391 0525

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1280 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 63..1172

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AGCTCCAGCC TAGGCGTTCT ACCTGGAAGA ATGCAGGGGC CCAGTACCTA GGACTGAGGA 60
AG ATG GCT GAC ATC CAG AAC ATT TCG CTG GAC AGC CCA GGG AGC GTA 107

Applicants: Jonathan A. Bard et al.
Serial No: Not Yet Known
Filed: Herewith
Exhibit 2

Met	Ala	Asp	Ile	Gln	Asn	Ile	Ser	Leu	Asp	Ser	Pro	Gly	Ser	Val		
1				5					10					15		
GGG	GCT	GTG	GCA	GTG	CCT	GTG	ATC	TTT	GCC	CTC	ATC	TTC	CTG	TTG	GGC	155
Gly	Ala	Val	Ala	Val	Pro	Val	Ile	Phe	Ala	Leu	Ile	Phe	Leu	Leu	Gly	
				20					25					30		
ATG	GTG	GGC	AAT	GGG	CTG	GTG	TTG	GCT	GTG	CTA	CTG	CAG	CCT	GGC	CCA	203
Met	Val	Gly	Asn	Gly	Leu	Val	Leu	Ala	Val	Leu	Leu	Gln	Pro	Gly	Pro	
			35					40					45			
AGT	GCC	TGG	CAG	GAG	CCA	AGC	AGT	ACC	ACA	GAT	CTC	TTC	ATC	CTC	AAC	251
Ser	Ala	Trp	Gln	Glu	Pro	Ser	Ser	Thr	Thr	Asp	Leu	Phe	Ile	Leu	Asn	
		50					55					60				
TTG	GCC	GTG	GCC	GAC	CTT	TGC	TTC	ATC	CTG	TGC	TGC	GTG	CCC	TTC	CAG	299
Leu	Ala	Val	Ala	Asp	Leu	Cys	Phe	Ile	Leu	Cys	Cys	Val	Pro	Phe	Gln	
	65					70					75					
GCA	GCC	ATC	TAC	ACA	CTG	GAT	GCC	TGG	CTC	TTT	GGG	GCT	TTC	GTG	TGC	347
Ala	Ala	Ile	Tyr	Thr	Leu	Asp	Ala	Trp	Leu	Phe	Gly	Ala	Phe	Val	Cys	
	80				85					90					95	
AAG	ACG	GTA	CAT	CTG	CTC	ATC	TAC	CTC	ACC	ATG	TAT	GCC	AGC	AGC	TTC	395
Lys	Thr	Val	His	Leu	Leu	Ile	Tyr	Leu	Thr	Met	Tyr	Ala	Ser	Ser	Phe	
			100						105					110		
ACC	CTG	GCG	GCC	GTC	TCC	CTG	GAC	AGG	TAC	CTG	GCT	GTG	CGG	CAC	CCA	443
Thr	Leu	Ala	Ala	Val	Ser	Leu	Asp	Arg	Tyr	Leu	Ala	Val	Arg	His	Pro	
			115					120					125			
CTG	CGC	TCC	AGA	GCC	CTG	CGC	ACC	CCG	CGC	AAC	GCG	CGC	GCC	GCC	GTG	491
Leu	Arg	Ser	Arg	Ala	Leu	Arg	Thr	Pro	Arg	Asn	Ala	Arg	Ala	Ala	Val	
		130					135					140				
GGG	CTC	GTG	TGG	CTG	CTG	GCG	GCT	CTC	TTT	TCC	GCG	CCC	TAC	CTA	AGC	539
Gly	Leu	Val	Trp	Leu	Leu	Ala	Ala	Leu	Phe	Ser	Ala	Pro	Tyr	Leu	Ser	
	145					150					155					
TAT	TAC	GGC	ACG	GTG	CGC	TAC	GGC	GCG	CTC	GAG	CTC	TGC	GTG	CCC	GCT	587
Tyr	Tyr	Gly	Thr	Val	Arg	Tyr	Gly	Ala	Leu	Glu	Leu	Cys	Val	Pro	Ala	
	160				165					170					175	
TGG	GAG	GAC	GCG	CGG	CGG	CGC	GCG	CTG	GAC	GTG	GCC	ACC	TTC	GCC	GCG	635
Trp	Glu	Asp	Ala	Arg	Arg	Arg	Ala	Leu	Asp	Val	Ala	Thr	Phe	Ala	Ala	
				180					185					190		
GGC	TAC	CTG	CTG	CCG	GTG	GCC	GTG	GTG	AGC	CTG	GCC	TAC	GGA	CGC	ACG	683
Gly	Tyr	Leu	Leu	Pro	Val	Ala	Val	Val	Ser	Leu	Ala	Tyr	Gly	Arg	Thr	
			195					200					205			
CTA	TGT	TTC	CTA	TGG	GCC	GCC	GTG	GGT	CCC	GCG	GGC	GCG	GCG	GCA	GCA	731
Leu	Cys	Phe	Leu	Trp	Ala	Ala	Val	Gly	Pro	Ala	Gly	Ala	Ala	Ala	Ala	
			210				215					220				
GAG	GCG	CGC	AGA	CGG	GCG	ACC	GGC	CGG	GCG	GGA	CGC	GCC	ATG	CTG	GCA	779
Glu	Ala	Arg	Arg	Arg	Ala	Thr	Gly	Arg	Ala	Gly	Arg	Ala	Met	Leu	Ala	
	225					230					235					
GTG	GCC	GCG	CTC	TAC	GCG	CTT	TGC	TGG	GCG	CCG	CAC	CAC	GCG	CTC	ATC	827
Val	Ala	Ala	Leu	Tyr	Ala	Leu	Cys	Trp	Gly	Pro	His	His	Ala	Leu	Ile	
	240				245					250					255	

CTC TGC TTC TGG TAC GGC CGC TTC GCC TTC AGC CCG GCC ACC TAC GCC	875
Leu Cys Phe Trp Tyr Gly Arg Phe Ala Phe Ser Pro Ala Thr Tyr Ala	
260 265 270	
TGT CGC CTG GCC TCG CAC TGC CTC GCC TAC GCC AAC TCC TGC CTT AAC	923
Cys Arg Leu Ala Ser His Cys Leu Ala Tyr Ala Asn Ser Cys Leu Asn	
275 280 285	
CCG CTC GTC TAC TCG CTC GCC TCG CGC CAC TTC CGC GCG CGC TTC CGC	971
Pro Leu Val Tyr Ser Leu Ala Ser Arg His Phe Arg Ala Arg Phe Arg	
290 295 300	
CGC CTG TGG CCC TGC GGC CGT CGC CGC CAC CGC CAC CAC CAC CGC GCT	1019
Arg Leu Trp Pro Cys Gly Arg Arg Arg His Arg His His His Arg Ala	
305 310 315	
CAT CGA GCC CTC CGT CGT GTC CAG CCG GCG TCT TCG GGC CCC GCC GGT	1067
His Arg Ala Leu Arg Arg Val Gln Pro Ala Ser Ser Gly Pro Ala Gly	
320 325 330 335	
TAT CCC GGC GAC GCC AGG CCT CGT GGT TGG AGT ATG GAG CCC AGA GGG	1115
Tyr Pro Gly Asp Ala Arg Pro Arg Gly Trp Ser Met Glu Pro Arg Gly	
340 345 350	
GAT GCT CTG CGT GGT GGT GGA GAG ACT AGA CTA ACC CTG TCC CCC AGG	1163
Asp Ala Leu Arg Gly Gly Gly Glu Thr Arg Leu Thr Leu Ser Pro Arg	
355 360 365	
GGA CCT CAA TAACCCCTGCC CGCTTGGA CTGACGTCTG TCAGAATGCC	1212
Gly Pro Gln	
370	
ACCAAGGAAC ATCTAGGGAA CGGCAGTCTC GCCAGGCTCC ACCAAAAAGC AGAAGCAAAG	1272
TTGCAGGG	1280

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 370 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ala Asp Ile Gln Asn Ile Ser Leu Asp Ser Pro Gly Ser Val Gly	
1 5 10 15	
Ala Val Ala Val Pro Val Ile Phe Ala Leu Ile Phe Leu Leu Gly Met	
20 25 30	
Val Gly Asn Gly Leu Val Leu Ala Val Leu Leu Gln Pro Gly Pro Ser	
35 40 45	
Ala Trp Gln Glu Pro Ser Ser Thr Thr Asp Leu Phe Ile Leu Asn Leu	
50 55 60	
Ala Val Ala Asp Leu Cys Phe Ile Leu Cys Cys Val Pro Phe Gln Ala	
65 70 75 80	

Ala	Ile	Tyr	Thr	Leu	Asp	Ala	Trp	Leu	Phe	Gly	Ala	Phe	Val	Cys	Lys
				85					90					95	
Thr	Val	His	Leu	Leu	Ile	Tyr	Leu	Thr	Met	Tyr	Ala	Ser	Ser	Phe	Thr
			100					105					110		
Leu	Ala	Ala	Val	Ser	Leu	Asp	Arg	Tyr	Leu	Ala	Val	Arg	His	Pro	Leu
		115					120					125			
Arg	Ser	Arg	Ala	Leu	Arg	Thr	Pro	Arg	Asn	Ala	Arg	Ala	Ala	Val	Gly
	130					135					140				
Leu	Val	Trp	Leu	Leu	Ala	Ala	Leu	Phe	Ser	Ala	Pro	Tyr	Leu	Ser	Tyr
145					150					155					160
Tyr	Gly	Thr	Val	Arg	Tyr	Gly	Ala	Leu	Glu	Leu	Cys	Val	Pro	Ala	Trp
				165					170					175	
Glu	Asp	Ala	Arg	Arg	Arg	Ala	Leu	Asp	Val	Ala	Thr	Phe	Ala	Ala	Gly
			180					185					190		
Tyr	Leu	Leu	Pro	Val	Ala	Val	Val	Ser	Leu	Ala	Tyr	Gly	Arg	Thr	Leu
	195						200					205			
Cys	Phe	Leu	Trp	Ala	Ala	Val	Gly	Pro	Ala	Gly	Ala	Ala	Ala	Ala	Glu
	210					215					220				
Ala	Arg	Arg	Arg	Ala	Thr	Gly	Arg	Ala	Gly	Arg	Ala	Met	Leu	Ala	Val
225					230					235					240
Ala	Ala	Leu	Tyr	Ala	Leu	Cys	Trp	Gly	Pro	His	His	Ala	Leu	Ile	Leu
				245					250					255	
Cys	Phe	Trp	Tyr	Gly	Arg	Phe	Ala	Phe	Ser	Pro	Ala	Thr	Tyr	Ala	Cys
			260					265					270		
Arg	Leu	Ala	Ser	His	Cys	Leu	Ala	Tyr	Ala	Asn	Ser	Cys	Leu	Asn	Pro
	275						280					285			
Leu	Val	Tyr	Ser	Leu	Ala	Ser	Arg	His	Phe	Arg	Ala	Arg	Phe	Arg	Arg
	290					295					300				
Leu	Trp	Pro	Cys	Gly	Arg	Arg	His	Arg	His	His	His	Arg	Ala	His	
305					310				315					320	
Arg	Ala	Leu	Arg	Arg	Val	Gln	Pro	Ala	Ser	Ser	Gly	Pro	Ala	Gly	Tyr
				325					330					335	
Pro	Gly	Asp	Ala	Arg	Pro	Arg	Gly	Trp	Ser	Met	Glu	Pro	Arg	Gly	Asp
			340					345					350		
Ala	Leu	Arg	Gly	Gly	Gly	Glu	Thr	Arg	Leu	Thr	Leu	Ser	Pro	Arg	Gly
		355					360					365			
Pro	Gln														
	370														

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1417 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 1..1281

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CAC	TCA	GCG	ATG	ACT	TTG	GCT	CTG	CTC	TCC	CCT	CCT	CCA	TCT	CCC	ACG	48
His	Ser	Ala	Met	Thr	Leu	Ala	Leu	Leu	Ser	Pro	Pro	Pro	Ser	Pro	Thr	
				375					380					385		
AGC	TTC	CAG	CCC	AGA	ACA	CCT	GGC	CAG	ACC	CAG	GTC	GGG	GGA	GTT	AGA	96
Ser	Phe	Gln	Pro	Arg	Thr	Pro	Gly	Gln	Thr	Gln	Val	Gly	Gly	Val	Arg	
			390					395					400			
TCC	CGG	GGT	CAA	GCA	ACC	AGA	ACT	GGG	GGC	TCT	TGC	CTG	AGG	ATT	CCA	144
Ser	Arg	Gly	Gln	Ala	Thr	Arg	Thr	Gly	Gly	Ser	Cys	Leu	Arg	Ile	Pro	
		405					410					415				
GCT	TCT	CTT	CCC	AGG	TGC	CCG	TCT	GAT	GGG	GAG	ATG	GCT	GAT	GCC	CAG	192
Ala	Ser	Leu	Pro	Arg	Cys	Pro	Ser	Asp	Gly	Glu	Met	Ala	Asp	Ala	Gln	
		420				425					430					
AAC	ATT	TCA	CTG	GAC	AGC	CCA	GGG	AGT	GTG	GGG	GCC	GTG	GCA	GTG	CCT	240
Asn	Ile	Ser	Leu	Asp		Pro	Gly	Ser	Val	Gly	Ala	Val	Ala	Val	Pro	
		435			440					445					450	
GTG	GTC	TTT	GCC	CTA	ATC	TTC	CTG	CTG	GGC	ACA	GTG	GGC	AAT	GGG	CTG	288
Val	Val	Phe	Ala	Leu	Ile	Phe	Leu	Leu	Gly	Thr	Val	Gly	Asn	Gly	Leu	
			455						460					465		
GTG	CTG	GCA	GTG	CTC	CTG	CAG	CCT	GGC	CCG	AGT	GCC	TGG	CAG	GAG	CCT	336
Val	Leu	Ala	Val	Leu	Leu	Gln	Pro	Gly	Pro	Ser	Ala	Trp	Gln	Glu	Pro	
			470					475					480			
GGC	AGC	ACC	ACG	GAC	CTG	TTC	ATC	CTC	AAC	CTG	GCG	GTG	GCT	GAC	CTC	384
Gly	Ser	Thr	Thr	Asp	Leu	Phe	Ile	Leu	Asn	Leu	Ala	Val	Ala	Asp	Leu	
		485					490					495				
TGC	TTC	ATC	CTG	TGC	TGC	GTG	CCC	TTC	CAG	GCC	ACC	ATC	TAC	ACG	CTG	432
Cys	Phe	Ile	Leu	Cys	Cys	Val	Pro	Phe	Gln	Ala	Thr	Ile	Tyr	Thr	Leu	
		500				505					510					
GAT	GCC	TGG	CTC	TTT	GGG	GCC	CTC	GTC	TGC	AAG	GCC	GTG	CAC	CTG	CTC	480
Asp	Ala	Trp	Leu	Phe	Gly	Ala	Leu	Val	Cys	Lys	Ala	Val	His	Leu	Leu	
		515			520				525					530		
ATC	TAC	CTC	ACC	ATG	TAC	GCC	AGC	AGC	TTT	ACG	CTG	GCT	GCT	GTC	TCC	528
Ile	Tyr	Leu	Thr	Met	Tyr	Ala	Ser	Ser	Phe	Thr	Leu	Ala	Ala	Val	Ser	
			535						540					545		
GTG	GAC	AGG	TAC	CTG	GCC	GTG	CGG	CAC	CCG	CTG	CGC	TCG	CGC	GCC	CTG	576
Val	Asp	Arg	Tyr	Leu	Ala	Val	Arg	His	Pro	Leu	Arg	Ser	Arg	Ala	Leu	
			550				555						560			
CGC	ACG	CCG	CGT	AAC	GCC	CGC	GCC	GCA	GTG	GGG	CTG	GTG	TGG	CTG	CTG	624

Arg	Thr	Pro	Arg	Asn	Ala	Arg	Ala	Val	Gly	Leu	Val	Trp	Leu	Leu		
565				570				575								
GCG Ala	GCG Ala	CTC Leu	TTC Phe	TCG Ser	GCG Ala	CCC Pro	TAC Tyr	CTC Leu	AGC Ser	TAC Tyr	TAC Tyr	GGC Gly	ACC Thr	GTG Val	CGC Arg	672
580				585				590								
TAC Tyr	GGC Gly	GCG Ala	CTG Leu	GAG Glu	CTC Leu	TGC Cys	GTG Val	CCC Pro	GCC Ala	TGG Trp	GAG Glu	GAC Asp	GCG Ala	CGC Arg	CGC Arg	720
595				600				605								
CGC Arg	GCC Ala	CTG Leu	GAC Asp	GTG Val	GCC Ala	ACC Thr	TTC Phe	GCT Ala	GCC Ala	GGC Gly	TAC Tyr	CTG Leu	CTG Leu	CCC Pro	GTG Val	768
610				615				620								
GCT Ala	GTG Val	GTG Val	AGC Ser	CTG Leu	GCC Ala	TAC Tyr	GGG Gly	CGC Arg	ACG Thr	CTG Leu	CGC Arg	TTC Phe	CTG Leu	TGG Trp	GCC Ala	816
630				635				640								
GCC Ala	GTG Val	GGT Gly	CCC Pro	GCG Ala	GGC Gly	GCG Ala	GCG Ala	GCC Ala	GAG Glu	GCG Ala	CGG Arg	CGG Arg	AGG Arg	GCG Ala		864
645				650				655								
ACG Thr	GGC Gly	CGC Arg	GCG Ala	GGG Gly	CGC Arg	GCC Ala	ATG Met	CTG Leu	GCG Ala	GTG Val	GCC Ala	GCG Ala	CTC Leu	TAC Tyr	GCG Ala	912
660				665				670								
CTC Leu	TGC Cys	TGG Trp	GGT Gly	CCG Pro	CAC His	CAC His	GCG Ala	CTC Leu	ATC Ile	CTG Leu	TGC Cys	TTC Phe	TGG Trp	TAC Tyr	GGC Gly	960
675				680				685								
CGC Arg	TTC Phe	GCC Ala	TTC Phe	AGC Ser	CCG Pro	GCC Ala	ACC Thr	TAC Tyr	GCC Ala	TGC Cys	CGC Arg	CTG Leu	GCC Ala	TCA Ser	CAC His	1008
695				700				705								
TGC Cys	CTG Leu	GCC Ala	TAC Tyr	GCC Ala	AAC Asn	TCC Ser	TGC Cys	CTC Leu	AAC Asn	CCG Pro	CTC Leu	GTC Val	TAC Tyr	GCG Ala	CTC Leu	1056
710				715				720								
GCC Ala	TCG Ser	CGC Arg	CAC His	TTC Phe	CGC Arg	GCG Ala	CGC Arg	TTC Phe	CGC Arg	CTG Leu	TGG Trp	CCG Pro	TGC Cys	GGC Gly		1104
725				730				735								
CGC Arg	CGA Arg	CGC Arg	CGC Arg	CAC His	CGT Arg	GCC Ala	CGC Arg	GCC Ala	TTG Leu	CGT Arg	CGC Arg	GTC Val	CGC Arg	CCC Pro		1152
740				745				750								
GCG Ala	TCC Ser	TCG Ser	GGC Gly	CCA Pro	CCC Pro	GGC Gly	TGC Cys	CCC Pro	GGA Gly	GAC Asp	GCC Ala	CGG Arg	CCT Pro	AGC Ser	GGG Gly	1200
755				760				765								
AGG Arg	CTG Leu	CTG Leu	GCT Ala	GGT Gly	GGC Gly	GGC Gly	CAG Gln	GGC Gly	CCG Pro	GAG Glu	CCC Pro	AGG Arg	GAG Glu	GGA Gly	CCC Pro	1248
775				780				785								
GTC Val	CAC His	GGC Gly	GGA Gly	GAG Glu	GCT Ala	GCC Ala	CGA Arg	GGA Gly	CCG Pro	GAA Glu	TAAACCCTGC	CGCCTGGACT				1301
790				795												
CCGCCTGTGT CCGTCTGTCT CACTCCCGTT CTCCGAAGGC GGGACGCCAC CGGGCCAGGG																1361
ATGGGGCAAT GCCACGAGCT CTCTGAGGGG CGTTGAGTGG AGCGACTTGT CCCCCG																1417

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 427 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

His	Ser	Ala	Met	Thr	Leu	Ala	Leu	Leu	Ser	Pro	Pro	Pro	Ser	Pro	Thr	
1				5					10					15		
Ser	Phe	Gln	Pro	Arg	Thr	Pro	Gly	Gln	Thr	Gln	Val	Gly	Gly	Val	Arg	
			20					25					30			
Ser	Arg	Gly	Gln	Ala	Thr	Arg	Thr	Gly	Gly	Ser	Cys	Leu	Arg	Ile	Pro	
		35					40					45				
Ala	Ser	Leu	Pro	Arg	Cys	Pro	Ser	Asp	Gly	Glu	Met	Ala	Asp	Ala	Gln	
	50					55					60					
Asn	Ile	Ser	Leu	Asp	Ser	Pro	Gly	Ser	Val	Gly	Ala	Val	Ala	Val	Pro	
65					70					75					80	
Val	Val	Phe	Ala	Leu	Ile	Phe	Leu	Leu	Gly	Thr	Val	Gly	Asn	Gly	Leu	
				85					90					95		
Val	Leu	Ala	Val	Leu	Leu	Gln	Pro	Gly	Pro	Ser	Ala	Trp	Gln	Glu	Pro	
			100					105					110			
Gly	Ser	Thr	Thr	Asp	Leu	Phe	Ile	Leu	Asn	Leu	Ala	Val	Ala	Asp	Leu	
		115					120					125				
Cys	Phe	Ile	Leu	Cys	Cys	Val	Pro	Phe	Gln	Ala	Thr	Ile	Tyr	Thr	Leu	
	130					135					140					
Asp	Ala	Trp	Leu	Phe	Gly	Ala	Leu	Val	Cys	Lys	Ala	Val	His	Leu	Leu	
145					150					155					160	
Ile	Tyr	Leu	Thr	Met	Tyr	Ala	Ser	Ser	Phe	Thr	Leu	Ala	Ala	Val	Ser	
				165					170					175		
Val	Asp	Arg	Tyr	Leu	Ala	Val	Arg	His	Pro	Leu	Arg	Ser	Arg	Ala	Leu	
		180						185					190			
Arg	Thr	Pro	Arg	Asn	Ala	Arg	Ala	Ala	Val	Gly	Leu	Val	Trp	Leu	Leu	
		195					200					205				
Ala	Ala	Leu	Phe	Ser	Ala	Pro	Tyr	Leu	Ser	Tyr	Tyr	Gly	Thr	Val	Arg	
	210					215					220					
Tyr	Gly	Ala	Leu	Glu	Leu	Cys	Val	Pro	Ala	Trp	Glu	Asp	Ala	Arg	Arg	
225					230					235				240		
Arg	Ala	Leu	Asp	Val	Ala	Thr	Phe	Ala	Ala	Gly	Tyr	Leu	Leu	Pro	Val	
				245					250					255		
Ala	Val	Val	Ser	Leu	Ala	Tyr	Gly	Arg	Thr	Leu	Arg	Phe	Leu	Trp	Ala	
			260					265					270			

Ala Val Gly Pro Ala Gly Ala Ala Ala Glu Ala Arg Arg Arg Ala
 275 280 285

Thr Gly Arg Ala Gly Arg Ala Met Leu Ala Val Ala Ala Leu Tyr Ala
 290 295 300

Leu Cys Trp Gly Pro His His Ala Leu Ile Leu Cys Phe Trp Tyr Gly
 305 310 315 320

Arg Phe Ala Phe Ser Pro Ala Thr Tyr Ala Cys Arg Leu Ala Ser His
 325 330 335

Cys Leu Ala Tyr Ala Asn Ser Cys Leu Asn Pro Leu Val Tyr Ala Leu
 340 345 350

Ala Ser Arg His Phe Arg Ala Arg Phe Arg Arg Leu Trp Pro Cys Gly
 355 360 365

Arg Arg Arg Arg His Arg Ala Arg Arg Ala Leu Arg Arg Val Arg Pro
 370 375 380

Ala Ser Ser Gly Pro Pro Gly Cys Pro Gly Asp Ala Arg Pro Ser Gly
 385 390 395 400

Arg Leu Leu Ala Gly Gly Gly Gln Gly Pro Glu Pro Arg Glu Gly Pro
 405 410 415

Val His Gly Gly Glu Ala Ala Arg Gly Pro Glu
 420 425

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 346 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Glu Leu Ala Pro Val Asn Leu Ser Glu Gly Asn Gly Ser Asp Pro
 1 5 10 15

Glu Pro Pro Ala Glu Pro Arg Pro Leu Phe Gly Ile Gly Val Glu Asn
 20 25 30

Phe Ile Thr Leu Val Val Phe Gly Leu Ile Phe Ala Met Gly Val Leu
 35 40 45

Gly Asn Ser Leu Val Ile Thr Val Leu Ala Arg Ser Lys Pro Gly Lys
 50 55 60

Pro Arg Ser Thr Thr Asn Leu Phe Ile Leu Asn Leu Ser Ile Ala Asp
 65 70 75 80

Leu Ala Tyr Leu Leu Phe Cys Ile Pro Phe Gln Ala Thr Val Tyr Ala
 85 90 95

Leu Pro Thr Trp Val Leu Gly Ala Phe Ile Cys Lys Phe Ile His Tyr

100					105					110					
Phe	Phe	Thr	Val	Ser	Met	Leu	Val	Ser	Ile	Phe	Thr	Leu	Ala	Ala	Met
		115					120					125			
Ser	Val	Asp	Arg	Tyr	Val	Ala	Ile	Val	His	Ser	Arg	Arg	Ser	Ser	Ser
		130				135					140				
Leu	Arg	Val	Ser	Arg	Asn	Ala	Leu	Leu	Gly	Val	Gly	Phe	Ile	Trp	Ala
		145				150					155				160
Leu	Ser	Ile	Ala	Met	Ala	Ser	Pro	Val	Ala	Tyr	Tyr	Gln	Arg	Leu	Phe
				165					170					175	
His	Arg	Asp	Ser	Asn	Gln	Thr	Phe	Cys	Trp	Glu	His	Trp	Pro	Asn	Gln
			180					185					190		
Leu	His	Lys	Lys	Ala	Tyr	Val	Val	Cys	Thr	Phe	Val	Phe	Gly	Tyr	Leu
		195					200					205			
Leu	Pro	Leu	Leu	Leu	Ile	Cys	Phe	Cys	Tyr	Ala	Lys	Val	Leu	Asn	His
		210				215					220				
Leu	His	Lys	Lys	Leu	Lys	Asn	Met	Ser	Lys	Lys	Ser	Glu	Ala	Ser	Lys
		225				230					235				240
Lys	Lys	Thr	Ala	Gln	Thr	Val	Leu	Val	Val	Val	Val	Val	Phe	Gly	Ile
				245					250					255	
Ser	Trp	Leu	Pro	His	His	Val	Ile	His	Leu	Trp	Ala	Glu	Phe	Gly	Ala
			260					265					270		
Phe	Pro	Leu	Thr	Pro	Ala	Ser	Phe	Phe	Phe	Arg	Ile	Thr	Ala	His	Cys
		275					280					285			
Leu	Ala	Tyr	Ser	Asn	Ser	Ser	Val	Asn	Pro	Ile	Ile	Tyr	Ala	Phe	Leu
		290				295					300				
Ser	Glu	Asn	Phe	Arg	Lys	Ala	Tyr	Lys	Gln	Val	Phe	Lys	Cys	Arg	Val
		305				310					315				320
Cys	Asn	Glu	Ser	Pro	His	Gly	Asp	Ala	Lys	Glu	Lys	Asn	Arg	Ile	Asp
				325					330					335	
Thr	Pro	Pro	Ser	Thr	Asn	Cys	Thr	His	Val						
			340					345							

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TTGTACCCCT ATTTTTCGCG CTCATCTTCC TCGTGGGCAC CGTGG

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AGCACCGCCA GCACCAGCGC GTTGCCACG GTGCCACGA GGAAG

45

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TCAGCACCAC CAACCTGTTC ATCCTCAACC TGGGCGTGGC CGACCTGTGT

50

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GGCCTGGAAA GGCACGCAGC ACAGGATGAA ACACAGGTCG GCCACGCCCA

50

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CTGCAAGGCT GTTCATTCC TCATCTTTCT CACTATGCAC GCCAG

45

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GGAGACGGCG GCCAGCGTGA AGCTGCTGGC GTGCATAGTG AGAAA

45

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

AACGCGCTGG CCGCCATCGG GCTCATCTGG GGGCTAGCAC TGCTC

45

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

AGTAGCTCAG GTAGGGCCCG GAGAAGAGCA GTGCTAGCCC CCAGA

45

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

AGCCATGGAC CTCTGCACCT TCGTCTTTAG CTACCTGCTG CCAGT

45

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CGCATAGGTC AGACTGAGGA CTAGCACTGG CAGCAGGTAG CTAAG

45

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GATCATCATC GTGGCGGTGC TTTTCTGCCT CTGTTGGATG CCCCCA

45

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CCACACGCAG AGGATAAGCG CGTGGTGGGG CATCCAACAG AGGCA

45

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GTTGCGCATC CTTTCACACC TAGTTTCCTA TGCCAACTCC TGTGT

45

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

AGACCAGAGC GTAAACGATG GGGTTGACAC AGGAGTTGGC ATAGGA

46

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CCTCAGTGAA GGAATGGGA GCGA

24

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GTAGTGTATA AACTTGCAGA TGAAGGC

27

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

ATGAATGGCT CCGGCAGCCA GGG

23

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

TTGCAGAGCA GCGAGCCGAA CAC

23

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GGCTGACATC CAGAACATTT CGCT

24

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CAGATGTACC GTCTTGACA CGAA

24

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

CATCTGCTCA TCTACCTCAC CATG

24

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CATAGGAAAC ATAGCGTGCG TCCG

24

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

AAGCTTCTAG AGATCCCTCG ACCTC

25

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

AGGCGCAGAA CTGGTAGGTA TGGAA

25

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GCTCATCCTC TGCTTCTGGT ACG

23

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

CAGATGTACC GTCTTGCACA CGAA

24

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 34 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CGAGGATCCC AACTTTGCCT CTGCTTTTTG GTGG

34

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CCTCAGTGAA GGGAATGGGA GCGA

24

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

CTTGCTTGTA CGCCTTCCGG AAGT

24

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

TGGGCAACAG CCTAGTGATC ACCG

24

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

CTGCTCCCAG CAGAAGGTCT GGTT

24

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

ATGAATGGCT CCGGCAGCCA GGG

23

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

TTGGAGACCA GAGCGTAAAC GATGG

25

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

AGATGGCTGA CATCCAGAAC ATTCGCTGG ACAGCCCAGG GAGCG

45

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 46 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

ATCACAGGCA CTGCCACAGC CCCTACGCTC CCTGGGCTGT CCAGCG

46

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

ATGGCTGATG CCCAGAACAT TTCAC

25

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

AGCCAGGCAT CCAGCGTGTA GAT

23

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

ACGGTCGCTT CGCCTTCAGC CCGGCCACCT ACGCCTGTG CCGG

45

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

ACGGTCGCTT CGCCTTCAGC CCGGCCACCT ACGCCTGTCG CCTGG

45

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

GCGCAACGCG CGCGCCGCCG TGGGGCTCGT GTGGCTGCTG GCGGC

45

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

ATCTACACGC TGGATGCCTG GCTCTTTGGG GCCCTCGTCT GCAAG

45

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

ATCTACACGC TGGATGCCCT GGCT

24

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

CGTAGCGCAC GGTGCCGTAG TA

22

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

GATGGATCCG CCACCATGGC TGATGCCAG AACATTTCAC

40

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

GCAGGTACCT GTCCACGGAG ACAGCAGC

28

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

GATGGCTGAT GCCAGAACA TTTCCTGGA CAGCCCAGGG AGTGT

45

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

GACCACAGGC ACTGCCACGG CCCCCACACT CCCTGGGCTG TCCAG

45

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

TGCAGCCTGG CCAAGTGCC TGGCAGGAGC CAAGCAGTAC CACAG

45

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

CGCGGATCCA TTATGTCTGC ACTCCGAAGG AAATTTG

37

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

CGCGAATTCT TATGTGAAGC GATCAGAGTT CATTTTTTC

38

(2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

GCGGGATCCG CTATGGCTGG TGATTCTAGG AATG

34

(2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

CCGGAATTCC CCTCACACCG AGCCCCTGG

29

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

CCAAGCTTCT AATACGACTC ACTATAGGGC CACCATGGCT GATGCCCAGA

50

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 57 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTGCAGG GTTTATCCG GTCCTCG

57

(2) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

TCAGCGGCAC CATGAACGTC TCGGGCT

27

(2) INFORMATION FOR SEQ ID NO:61:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

GGCCACATCA ACCGTCAGGA TGCT

24

(2) INFORMATION FOR SEQ ID NO:62:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

ATGGCTGATG CCCAGAACAT TTCAC

25

(2) INFORMATION FOR SEQ ID NO:63:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

TAGCGCACGG TGCCGTAGTA GCTGAGGT

28

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

ATGAAAGGGT CCCTCCTGCT GCTGCT

26

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

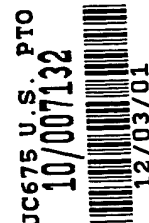
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

TATCAGCTCC ATGCCCTCTA GAAGCC

26

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicants : Jonathan A. Bard, et al.
Serial No. : 09/058,333
Filed : April 9, 1998
For : DNA ENCODING GALANIN GALR3 RECEPTOR AND USES
THEREOF



1185 Avenue of the Americas
New York, New York 10036
August 3, 1998

Assistant Commissioner for Patents
Washington, D.C. 20231
Box: Missing Parts


Sir:

STATEMENT IN ACCORDANCE WITH 37 C.F.R. §1.821(f)

In accordance with 37 C.F.R. §1.821(f), I hereby certify that the computer readable form containing the nucleic acid and/or amino acid sequences required by 37 C.F.R. §1.821(e) and submitted in connection with the above-identified application, has the same information as replacement pages 171-194 of the subject application entitled "Sequence Listing."

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these were made with the knowledge that wilful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such wilful false statements may jeopardize the validity of the application or any patent issued thereon.

Respectfully submitted,


Kimberly D. Branch
c/o Cooper & Dunham LLP
1185 Avenue of the Americas
New York, New York 10036
(212) 278-0400

Applicants: Jonathan A. Bard et al.
Serial No: Not Yet Known
Filed: Herewith
Exhibit 3

ATCC

10801 University Blvd • Manassas, VA 20110-2209 • Telephone: 703-365-2700 • FAX: 703-

BUDAPEST TREATY ON THE INTERNATIONAL RECOGNITION OF THE DEPOSIT OF MICROORGANISMS FOR THE PURPOSES OF PATENT PROCEDURE

INTERNATIONAL FORM

RECEIPT IN THE CASE OF AN ORIGINAL DEPOSIT ISSUED PURSUANT TO RULE 7.3
AND VIABILITY STATEMENT ISSUED PURSUANT TO RULE 10.2

JC675 U.S. PTO
10/007132
12/03/01

To: (Name and Address of Depositor or Attorney)

Cooper & Dunham LLP
Attn: John P. White, Esq.
1185 Avenue of the Americas
New York, NY 10036

COPY

Deposited on Behalf of: Synaptic Pharmaceutical Corporation (Docket 52241-E)

Identification Reference by Depositor:

ATCC Designation

Plasmid M67

209708

The deposit was accompanied by: a scientific description a proposed taxonomic description indicated above.

The deposit was received March 27, 1998 by this International Depository Authority and has been accepted.

AT YOUR REQUEST: X We will inform you of requests for the strain for 30 years.

The strain will be made available if a patent office signatory to the Budapest Treaty certifies one's right to receive, or if a U.S. Patent is issued citing the strain, and ATCC is instructed by the United States Patent & Trademark Office or the depositor to release said strain.

If the culture should die or be destroyed during the effective term of the deposit, it shall be your responsibility to replace it with living culture of the same.

The strain will be maintained for a period of at least 30 years from date of deposit, or five years after the most recent request for a sample, whichever is longer. The United States and many other countries are signatory to the Budapest Treaty.

The viability of the culture cited above was tested April 8, 1998. On that date, the culture was viable.

International Depository Authority: American Type Culture Collection, Manassas, VA 20110-2209 USA.

Signature of person having authority to represent ATCC:

Barbara M. Hailey
Barbara M. Hailey, Administrator, Patent Depository

Date: April 22, 1998

cc: Kimberly Branch

Applicants: Jonathan A. Bard et al.
Serial No: Not Yet Known
Filed: Herewith
Exhibit 4

Form PTO-1449

U.S. Department of Commerce
Patent and Trademark OfficeAtty. Docket No.
52241-EC
/JPW/ADM/PLSerial No.
Not Yet KnownINFORMATION DISCLOSURE CITATION
BY APPLICANT

(Use several sheets if necessary)

Applicant
Jonathan A. Bard, et al.Filing Date
Herewith

Group

JC675 U.S. PTO
10/007132
12/03/01

U.S. PATENT DOCUMENTS

Examiner Initial	Document Number	Date	Name	Class	Subclass	Filing Date if Appropriate
	5 2 9 0 8 0 8	3/1/94	Sofia, et al.			
	5 4 3 6 1 2 8	7/25/95	Harpold, et al.			
	5 4 3 6 1 5 5	7/25/95	Bell, et al.			
	5 4 6 2 8 5 6	10/31/95	Lerner, et al.			
	5 5 0 8 1 6 4	4/16/96	Kausch, et al.			
	5 5 6 7 7 1 4	10/22/96	Bruns, et al.			
	5 5 7 6 2 9 6	11/29/96	Bartfai, et al.			

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Document Number	Date	Country	Class	Subclass	Translation	
					Yes	No
9 9 3 1 1 3 0	6/24/99	PCT				
9 2 1 5 6 8 1	9/17/92	PCT				
9 8 0 3 5 4 8	1/29/98	PCT				
9 8 0 3 0 5 9	1/29/98	PCT				

OTHER DOCUMENTS (Including Author, Title, Date, Pertinent Pages, Etc.)

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EXAMINER

DATE CONSIDERED

*EXAMINER: Initial if reference considered, whether or not citation is in conformance with MPEP 609: Draw line through citation if not in conformance and not considered. Include copy of this form with next communication to applicant.

Applicants: Jonathan A. Bard et al.
 Serial No: Not Yet Known
 Filed: Herewith
 Exhibit 5

Form PTO-1449		U.S. Department of Commerce Patent and Trademark Office			Atty. Docket No. 52241-EC /JPW/ADM/PL		Serial No. Not Yet Known	
INFORMATION DISCLOSURE CITATION BY APPLICANT (Use several sheets if necessary)					Applicant Jonathan A. Bard, et al.			
					Filing Date Herewith		Group	

FOREIGN PATENT DOCUMENTS														
		Document Number							Date	Country	Class	Subclass	Translation	
													Yes	No
		9	2	1	2	9	9	7	8/6/92	PCT				
		9	2	1	5	0	1	5	9/3/92	PCT				
		9	5	2	2	6	0	8	8/24/95	PCT				
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		5	1	4	3	6	1		11/19/92	EPO				
		7	1	1	8	3	0		5/15/96	EPO				

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				Filing Date Herewith	Group
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EXAMINER			DATE CONSIDERED		
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	Applicant Jonathan A. Bard, et al.	
	Filing Date Herewith	Group

OTHER DOCUMENTS (Including Author, Title, Date, Pertinent Pages, Etc.)

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